

IN THE CLAIMS:

Claim 19 has been amended as follows:

1 19. (Twice Amended) Use of [the] a recombinant DNA molecule [according to
2 claim 6] comprising a promintron sequence of the rolA gene from *Agrobacterium*
3 *rhizogenes* as in SEQ ID NO. 1, or of DNA sequences comprising said promintron
4 sequence, or of functional homologous or portion thereof, to induce the expression of a
5 DNA coding sequence, in recombinant bacteria during exponential, post-exponential
6 and stationary phase of growth, and in bacteroids within root nodules, said coding DNA
7 sequence being under the control of said promintron sequence, said recombinant DNA
8 molecule being covalently linked to the 3' end of said promintron sequence, a DNA
9 coding sequence, said recombinant DNA molecule being either harboured by
10 prokaryotic episomal elements, or integrated in a bacterial genome to significantly
11 increase the plant biomass production.

The following new claim has been added:

1 21. (New) Use of a recombinant DNA molecule comprising a promintron
2 sequence of the rolA gene from *Agrobacterium rhizogenes* as in SEQ ID NO. 1, or of a
3 DNA coding sequence, or functional homologous or portion thereof, and covalently
4 linked to the 3' end of said promintron sequence, a DNA coding sequence, said
5 recombinant DNA molecule being either harboured by prokaryotic episomal elements,
6 or integrated in a bacterial genome to significantly increase the plant biomass
7 production.


8 sequence, said recombinant DNA molecule being either harboured by prokaryotic episomal
9 elements, or integrated in a bacterial genome to significantly increase the plant biomass
10 production.

Please add the following new claim:

1 22. Use of a recombinant DNA molecule comprising a promintron sequence of the rolA
2 gene from *Agrobacterium rhizogenes* as in SEQ ID NO. 1, or of a DNA coding sequence, or
3 functional homologous or portion thereof, and covalently linked to the 3' end of said promintron
4 sequence, a DNA coding sequence, said recombinant DNA molecule being either harboured by
5 prokaryotic episomal elements, or integrated in a bacterial genome to significantly increase the
6 plant biomass production.

Examination on the merits is respectfully requested.

Respectfully submitted,


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